

OM of: US-08-711-417C-165 to: Pending_Patents_AA_New:* out_format : pfs

Date: Aug 28, 2002 10:20 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q/cgn2_1/USPTO.spool/6228611/runat_28082002.10021113613/app_query.fasta_1.1639
-DB=Pending_Patents_AA_New -QFMT=fastan -SUFFIX=rapn
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000
-XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPEXT=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=blosom62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODAL
-OUTFMT=pfs -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=6228611 -CGN1_56 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-08-711-417C-165

Query length: 1551

Database: Pending_Patents_AA_New:*

Database sequences: 747981

Database length: 242050750

Search time (sec): 237.910000

score_list:

Sequence	Strd Orig	zScore	Escore	Len	Documentation
/cgn2_6/ptodata/1/paa/PCT_NEW_COMB.ppt:US02-09944-654		2551.50	2402.02	5.1e-126	
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.ppt:US-08-733-622C-25		2467.00	2323.17	1.4e-121	
/cgn2_6/ptodata/1/paa/US10_NEW_COMB.ppt:US-10-037-667-4		2458.50	2314.32	3.8e-121	
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.ppt:US-08-733-622C-27		2437.00	2294.05	5.0e-120	
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.ppt:US-08-733-622C-22		2207.50	2078.99	5.3e-108	
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.ppt:US-08-733-622C-26		1963.00	1849.71	3.4e-95	
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.ppt:US-08-733-622C-24		1923.50	1812.58	4.0e-93	
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.ppt:US-08-733-622C-23		1740.00	1642.00	1.6e-83	
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.ppt:US-08-733-622C-28		1681.00	1585.31	2.0e-80	
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.ppt:US-08-733-622C-29		1625.00	1532.93	1.7e-77	
/cgn2_6/ptodata/1/paa/US10_NEW_COMB.ppt:US-10-037-667-2		1360.50	1281.50	1.2e-63	
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.ppt:US-08-733-622C-2		1302.00	1226.86	1.4e-60	
/cgn2_6/ptodata/1/paa/US10_NEW_COMB.ppt:US-10-037-667-3		1301.00	1225.92	1.6e-60	
/cgn2_6/ptodata/1/paa/US10_NEW_COMB.ppt:US-10-037-667-1		1282.50	1208.08	1.5e-59	
/cgn2_6/ptodata/1/paa/US10_NEW_COMB.ppt:US-10-037-667-5		1126.00	1061.49	2.4e-51	
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.ppt:US-08-733-622C-31		965.00	916.01	6.4e-43	
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.ppt:US-08-733-622C-8		682.50	651.16	4.0e-38	
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.ppt:US-08-733-622C-37		668.50	638.03	2.2e-27	
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.ppt:US-08-733-622C-30		611.00	582.85	2.2e-24	
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.ppt:US-08-733-622C-36		605.00	577.43	4.6e-24	
/cgn2_6/ptodata/1/paa/PCT_NEW_COMB.ppt:US02-23913-321		395.50	375.87	4.3e-13	
/cgn2_6/ptodata/1/paa/US10_NEW_COMB.ppt:US-10-205-823-321		395.50	375.87	4.3e-13	
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.ppt:US-09-629-469A-14524		341.50	324.33	2.9e-10	
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.ppt:US-09-629-469A-18929		333.50	314.61	7.7e-10	
/cgn2_6/ptodata/1/paa/US06_NEW_COMB.ppt:US-60-389-987-1517		333.50	314.61	7.7e-10	
/cgn2_6/ptodata/1/paa/US06_NEW_COMB.ppt:US-60-389-987-527		331.50	312.52	9.8e-10	
/cgn2_6/ptodata/1/paa/US10_NEW_COMB.ppt:US-10-104-047-2937		331.00	310.38	1.0e-09	
/cgn2_6/ptodata/1/paa/US06_NEW_COMB.ppt:US-60-389-987-1850		330.00	308.88	1.2e-09	
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.ppt:US-08-733-622C-33		313.00	313.90	9.2e-09	
/cgn2_6/ptodata/1/paa/US06_NEW_COMB.ppt:US-60-389-987-2256		312.00	293.39	1.0e-08	
/cgn2_6/ptodata/1/paa/PCT_NEW_COMB.ppt:US02-21179-22		311.00	291.03	1.2e-08	
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.ppt:US-09-629-469A-14947		310.00	291.76	1.3e-08	
/cgn2_6/ptodata/1/paa/US10_NEW_COMB.ppt:US-10-144-194A-98		309.50	289.87	1.4e-08	
/cgn2_6/ptodata/1/paa/US10_NEW_COMB.ppt:US-10-144-194A-98		309.50	289.87	1.4e-08	
/cgn2_6/ptodata/1/paa/PCT_NEW_COMB.ppt:US02-09944-592		309.00	290.24	1.5e-08	
/cgn2_6/ptodata/1/paa/PCT_NEW_COMB.ppt:US02-09944-733		308.50	293.40	1.6e-08	
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.ppt:US-09-629-469A-18697		308.00	290.65	1.7e-08	
/cgn2_6/ptodata/1/paa/US10_NEW_COMB.ppt:US-10-007-280A-231		308.00	287.45	1.7e-08	
/cgn2_6/ptodata/1/paa/PCT_NEW_COMB.ppt:US02-21971-13		304.50	287.60	2.5e-08	
/cgn2_6/ptodata/1/paa/US06_NEW_COMB.ppt:US-60-389-987-2498		303.00	285.17	3.0e-08	

/cgn2_6/ptodata/1/paa/PCT_NEW_COMB.ppt:US02-10824-201 + 302.00 286.76 3.4e-08
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.ppt:US-09-629-469A-12631 + 302.00 286.76 3.4e-08
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.ppt:US-09-629-469A-12326 + 302.00 282.55 3.4e-08
/cgn2_6/ptodata/1/paa/US10_NEW_COMB.ppt:US-10-104-047-3671 + 301.00 288.07 3.9e-08
/cgn2_6/ptodata/1/paa/US06_NEW_COMB.ppt:US-60-389-987-2105 + 301.00 278.89 3.9e-08

seq_name: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.ppt:US02-09944-654

seq_documentation_block:

Sequence 654, Application PC/TUS0209944

GENERAL INFORMATION:

APPLICANT: INCYTE GENOMICS, INC.
DAFFO, Abel
JONES, Anissa L.
TRAN, Alanna-Phung B.
DAHL, Christopher R.
GIETZEN, Darryl
CHINN, Joyce
DUFOUR, Gerard E.
HILLMAN, Jennifer L.
YU, Jimmy Y.
TUASON, Olivia
YAP, Pierre E.
AMSHEY, Stefan R.
DAUGHERTY, Sean C.
DAM, Tam C.
LIU, Tommy F.
NGUYEN, Duy-Viet An
KLEEFELD, Yael
GERSTIN, JR., Edward H.
PERALTA, Careyna H.
DAVID, Marie H.
LEWIS, Samantha A.
CHEN, Alice J.
PANZER, Scott R.
HARRIS, Bernard
FLORES, Vincent
MARWAHA, Rakesh
LO, Audrey
LAN, Ruth Y.
TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
FILE REFERENCE: PT-1231 PCT
CURRENT APPLICATION NUMBER: PCT/US02/09944
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: 60/280,067; 60/279,619; 60/280,068; 60/291,280; 60/291,8
60/291,829; 60/299,428; 60/300,001; 60/299,776
PRIOR FILING DATE: 2001-03-29; 2001-03-28; 2001-03-29; 2001-05-16; 2001-05-17;
2001-05-17; 2001-06-19; 2001-06-20; 2001-06-20
NUMBER OF SEQ ID NOS: 792
SOFTWARE: PERL Program
SEQ ID NO 654
LENGTH: 499
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
OTHER INFORMATION: Incyte ID No: LI:345320.4.orf2:2001MAY17
PCT-US02-09944-654

alignment_scores:

Quality: 2551.50 Length: 498
Ratio: 5.186 Gaps: 3
Percent Similarity: 98.795 Percent Identity: 96.988

alignment_block:

US-08-711-417C-165 x PCT-US02-09944-654

Align seg 1/1 to: PCT-US02-09944-654 from: 1 to: 499

64 GATACCTCAGATGAGGCGATGACCCATGCGCATGCCGAGGACCTCTC 113
|||||

```
2  AspThrProAspGluGlyAspGluProMetProLeuProGluAspLeuSe 18
114 CACCACCTCGGGAGGACAGCAAGCTCCAAGAGTGACAGAGTCTGTGGCCA 163
115 rGluValValProValIleSerProMetTyrGlnLeuHisLysProLeuA 335
18 rThrThrSerGlyGlyGlnGlnSerLysSerAspArgValValAlas 35
164 GTAATGTTAAAGTAGACACTCAGAGTGATGAAGAGAAATGGCGTGTGT 213
165 rGluValValValValValValValValValValValValValValVal 351
35 erAsnValLysValGluThrGlnSerAspGluGluAsnGlyArgAlaCys 51
214 GAAATGAATGGGAAGAATGTCGGAGGATTACGAATGCTTGTATGCTC 263
52 GluMetAsnGlyGluGluCysAlaGluAspLeuArgMetLeuAspAlaSe 68
264 GGGAGAGAAAATGAATGGCTCCACAGAGGACCAAGGAGCTCGGCTTGT 313
68 rGlyGluLysMetAsnGlySerHisArgAspGlnGlySerSerAlaLeuS 85
314 CGGAGTGTGGAGGATTCGACTTCCTTACCGGAAACTAAAGTGTGATATC 363
85 erGlyValGlyGlyIleArgLeuProAsnGlyLysLeuLysCysAspIle 101
364 TGTGGGATCATTTGCATCGGCGCCCAATGCTCATGCTTCCACAAAGAAG 413
102 CysGlyIleIleCysIleGlyProAsnValLeuMetValHisLysArgSe 118
414 CCACACTGGAGAACGGCCCTTCAGAGTCAATCAGTGGCGGCTCATPTCA 463
118 rHisThrGlyGluArgProPheGlnCysAsnGlnCysGlyAlaSerPheT 135
464 CCCAAGAGGCAACCTGCTCCGGCACATCAAGCTGCATTCGGGGAGAAG 513
135 hrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHisSerGlyGluLys 151
514 CCCTTCAATGCCACCTCTCCAACTAGCCCTGCCCGGAGGAGCGCCCT 563
152 ProPheLysCysHisLeuCysAsnTyrAlaCysArgArgAspAlaLe 168
564 CACTGGCCACCTAGGACGACCTCCGTTGGTAAACCTCAACAAATGTGGAT 613
168 uThrGlyHisLeuArgThrHisSerValGlyLysProHisLysCysGlyT 185
614 ATTGTGCGGCAAGCTATAACAGGAACTGCTTTTAGAGGAACATAAAGAG 663
185 yrCysGlyArgSerTyrLysGlnArgSerSerLeuGluGluHisLysGlu 201
664 CGCTGCCACACTACTTGGAAAGCATGGGCTTCCGGGCACACTGTACCC 713
202 ArgCysHisAsnTyrLeuGluSerMetGlyLeuProGlyThrLeuTyrPr 218
714 AGTCATTAAAGAAAGAACTAAGCACACAGTGAATGGCAGAAAGACTGTGCA 763
218 oValIleLysGluGluThrAsnHisSerGluMetAlaGluAspLeuCysL 235
764 AGATAGGATCAGAGAGATCTCTGCTGCTGACACACTAGCAAGTAATGTC 813
235 ystIleGlySerGluArgSerLeuValLeuAspArgLeuAlaSerAsnVal 251
814 GCCAAAGTAAGAGCTATGCTCCTCAGAAATTTCTGGGCACAGGCGCT 863
252 AlaLysArgLysSerMetProGlnLysPheLeuGlyAspLysGlyLe 268
864 GTCGACACACCCCTAGCAC...AGTGCACGCTACGAGAAGGAAACGAAA 910
268 uSerAspThrProTyrAspSerSerAlaSerTyrGluLysGluAsnGluM 285
911 TGATGAAGTCCCAGGTGATGGACACAGCCATCAACACGCCATCAACTAC 960
285 etMetLysSerHisValMetAspGlnAlaIleAsnAsnAlaIleAsnTyr 301
961 CTGGGGCCGAGTCCCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1010
302 LeuGlyAlaGluSerLeuArgProLeuValGlnThrProProGlyGlySe 318
```

```
1011 CGAGGTGGTCCCGGTTCATCAGCCGATGTATCCAGTGCACAGG...CGCT 1057
1012 rGluValValProValIleSerProMetTyrGlnLeuHisLysProLeuA 335
1058 CGAGAGGACACCCCGCTCCAAACCACTCGCCCGCAGGACAGCGCGTGGAG 1107
1059 ::::~::~~::~~::~~::~~::~~::~~::~~::~~::~~::~~::~~::~~::
335 laGluGlyThrProArgSerAsnHisSerAlaGlnAspSerAlaValGlu 351
1108 TACTCTGCTGCTCTCCAAAGGCCAAGTTGTCCTCGGAGCGCGAGGC 1157
1109 ~::~~::~~::~~::~~::~~::~~::~~::~~::~~::~~::~~::~~::
352 AsnLeuLeuLeuLeuSerLysAlaLysLeuValProSerGluArgGluAl 368
1158 GTCCCCGAGCAACAGCTGCCAAGACTCCACGACACCGAGAGCAACAGC 1207
368 aSerProSerAsnSerCysGlnAspSerThrAspThrGluSerAsnAsnG 385
1208 AGAGACGAGCGCGGCTTATCTACCTGACCAACACATCGCCCGCAGCG 1257
1209 ~::~~::~~::~~::~~::~~::~~::~~::~~::~~::~~::~~::~~::
385 luGluGlnArgSerGlyLeuIleTyrLeuThrAsnHisIleAlaProHis 401
1258 GCACAAGC...GTGTCGCTCAAGGAGGACACGCGCCTACGACCTGCT 1304
1259 ~::~~::~~::~~::~~::~~::~~::~~::~~::~~::~~::~~::~~::
402 AlaArgAsnGlyLeuSerLeuLysGluLysHisArgAlaTyrAspLeuLe 418
1305 GCGCGCGCGCTCCGAGAACTCGCAGGACGCGCTCCGCTGGTGCAGACCA 1354
418 uArgAlaAlaSerGluAsnSerGlnAspAlaLeuArgValValSerThrS 435
1355 GCGGGGAGCAGATGAGGTGTACAAAGTGCAGAACACTCCCGGGTCTTTC 1404
435 erGlyGluGlnMetLysValTyrLysCysGluHisCysArgValLeuPhe 451
1405 CTGATCACGTCATGTACACCATCCACATGGCTGCCACGCTTCCGTGA 1454
1406 ~::~~::~~::~~::~~::~~::~~::~~::~~::~~::~~::~~::~~::
452 LeuAspHisValMetTyrThrIleHisMetGlyCysHisGlyPheArgAs 468
1455 TCCTTTTGTAGTCAACATGTGCGGTACCAAGCCAGCAGGACCGGTACGAGT 1504
468 pProPheGluCysAsnMetCysGlyTyrHisSerGlnAspArgTyrGluP 485
1505 TCTCGTCGCACATAACCGGAGGAGGACCGCTTCCACATGAGC 1548
485 heSerSerHisIleThrArgGlyGluHisArgPheHisMetSer 499
seq_name: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-25
seq_documentation_block:
; Sequence 25, Application US/08733622C
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia
; APPLICANT: Morgan, Bruce A.
; TITLE OF INVENTION: ATOLOS GENE
; FILE REFERENCE: 10287-030001
; CURRENT APPLICATION NUMBER: US/08/733,622C
; CURRENT FILING DATE: 1996-10-17
; PRIOR APPLICATION NUMBER: US 60/017,646
; PRIOR FILING DATE: 1996-05-14
; PRIOR APPLICATION NUMBER: US 60/005,529
; PRIOR FILING DATE: 1995-10-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-733-622C-25
```

```
alignment_scores:
  Quality: 2467.00      Length: 461
  Ratio: 5.351         Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
```

alignment_block:

US-08-711-417C-165 x US-08-733-622C-25

Align seg 1/1 to: US-08-733-622C-25 from: 1 to: 461

```

166 AATCTTAAGTAGAGACTCAGAGTGAAGAGAAATGGCGCTGCCCTGTGA 215
|||||
1 AsnValLysValGluThrGlnSerAspGluGluAsnGlyArgAlaCysGL 17
|||||
216 AATGAATGGGGAAGAATCTCGGAGGATTTACGAATGCTTGATGCTCGG 265
|||||
17 uMetAsnGlyGluGluCysAlaGluAspLeuArgMetLeuAspAlaSerG 34
|||||
266 GAGAGAAATGAATGGCTCCACAGGACCAAGGCAGCTCGGCTTGTGCG 315
|||||
34 LyGluLysMetAsnGlySerHisArgAspGlnGlySerSerAlaLeuSer 50
|||||
316 GGAGTTGGAGGCATTCGACTTCCTAAACGGAAACTAAAGTGTGATATCG 365
|||||
51 GlyValGlyGlyLeuArgLeuProAsnGlyLysLeuLysCysAspIleCy 67
|||||
366 TGGGATCATTTGTCATCGGCGCCCAATGTCTCATGTTTCACAAAAGAGCC 415
|||||
67 sGlyIleCysIleGlyProAsnValLeuMetValHisLysArgSerH 84
|||||
416 ACACCTGGAGAACGGCCTTCCAGTGAATCAGTGGCGGGCCTCATTCACC 465
|||||
84 iThrGlyGluArgProPheGlnCysAsnGlnCysGlyAlaSerPheThr 100
|||||
466 CAGAAGGGCAACCTGTCCGGGCACATCAAGCTGCATTCCGGGGAGAGCC 515
|||||
101 GlnLysGlyAsnLeuLeuArgHisIleLysLeuHisSerGlyGluLysPr 117
|||||
516 CTTCAAATGCCACCTCTGCACTACGCTTCCGCGCGGAGGACGCCCTCA 565
|||||
117 oPheLysCysHisLeuCysAsnTyrAlaCysArgArgAspAlaLeuT 134
|||||
566 CTGGCCACCTCAGGAGCGCACTCCGTGGTAAACCTTCACAAATGTGGAT 615
|||||
134 hrGlyHisLeuArgThrHisSerValGlyLysProHisLysCysGlyTyr 150
|||||
616 TGTGGCCGGAAGCTATAACAGCGAAGCTTTAGAGGAACATAAAGAGCG 665
|||||
151 CysGlyArgSerTyrLysGlnArgThrSerLeuGluHisLysGluAr 167
|||||
666 CTGCCACAACCTACTTGGAAAGCATGGGCTTCCGGGCACACTGTACCCAG 715
|||||
167 cCysHisAsnTyrLeuGluSerMetGlyLeuProGlyThrLeuTyrProV 184
|||||
716 TCATTAAGAGAAACTAAGCACAGTGAATGGCAGAAGACCTGTGCAAG 765
|||||
184 alileLysGluGluThrLysHisSerGluMetAlaGluAspLeuLys 200
|||||
766 ATAGGATCAGAGATCTCTGCTGTGACACACTAGCAAGTAATGTGCG 815
|||||
201 ileGlySerGluArgSerLeuValLeuAspArgLeuAlaSerAsnValAl 217
|||||
816 CAAACGTAAGAGCTCTATGCTCTCAGAAATTTCTGGGACACAGGCCCTGT 865
|||||
217 alySargLysSerSerMetProGlnLysPheLeuGlyAspLysGlyLeus 234
|||||
866 CGGACACGCCCTTACGACAGTCCCGACGTACGAGAGAGAGAAATGATG 915
|||||
234 eAspThrProTyrAspSerAlaThrTyrGluLysGluAsnGluMetMet 250
|||||
916 AAGTCCCGAGTGGACCAAGCATCAACAAACGCCCATCACTACCTGGG 965
|||||
251 LysSerHisValMetAspGlnAlaIleAsnAsnAlaIleAsnTyrLeuGL 267
|||||
966 GGCCGAGTCCCTCGCGCGCTGGTGGACAGCCCCCGGGCGGTTCGAGG 1015
|||||
267 yAlaGluSerLeuArgProLeuValGlnThrProGlyGlySerGluV 284

```

```

1016 TGGTCCCGGTCTATCAGCCCGATGTATCCAGCTGCACAGCGCTCGGAGGC 1065
|||||
284 alValProValIleSerProMetTyrGlnLeuHisArgSerGluGly 300
|||||
1066 ACCCGCGCTCCAAACACTCGGCCCGAGGACAGCGCGTGGAGTACTGCT 1115
|||||
301 ThrProArgSerAsnHisSerAlaGlnAspSerAlaValGluTyrLeuLe 317
|||||
1116 GTGTCTCTCCAAAGCCAAAGTTGGTCCCTCGGAGCGCGAGCGTCCCGGA 1165
|||||
317 uLeuLeuSerLysAlaLysLeuValProSerGluArgGluAlaSerProS 334
|||||
1166 GCAACAGCTGCCAAGACTCCACGGACACCGAGAGCAACAGAGAGAGCAG 1215
|||||
334 eAsnSerCysGlnAspSerThrAspThrGluSerAsnAsnGluGluGln 350
|||||
1216 CGCAGCGGTCTTATCTACCTGACCAACACATCGCCCGACGCGCGCAACG 1265
|||||
351 ArgSerGlyLeuIleTyrLeuThrAsnHisIleAlaArgArgAlaGlnAr 367
|||||
1266 CGTGTCTCAGGAGGAGACCGCGGCTACGACTGCTGTGCGCGCCGCT 1315
|||||
367 gValSerLeuLysGluGluHisArgAlaTyrAspLeuLeuArgAlaAla 384
|||||
1316 CCGAGAACTCGCAGGACGCGCTCCGCGTGTGTCAGCACCGCGGGGAGCAG 1365
|||||
384 erGluAsnSerGlnAspAlaLeuArgValSerThrSerGlyGluGln 400
|||||
1366 ATGAAGGTGTACAAGTGGAACTCGCGGTGCTCTTCTGTGATCACGT 1415
|||||
401 MetLysValTyrLysCysGluHisCysArgValLeuPheLeuAspHisVa 417
|||||
1416 CATGTACACCATCCACATGGGCTCCGCGCTTCCGTGATCCTTTTTCAGT 1465
|||||
417 lMetTyrThrIleHisMetGlyCysHisGlyPheArgAspProPheGluC 434
|||||
1466 GCAACATGTGCGGTACACAGCGAGCGGTCAGAGTTCGTCTGTCGCAC 1515
|||||
434 ysAsnMetCysGlyTyrHisSerGlnAspArgTyrGluPheSerSerHis 450
|||||
1516 ATAACGCGGAGGAGCACCGCTTCCACATGAGC 1548
|||||
451 lIleThrArgGlyGluHisArgPheHisMetSer 461

```

seq_name: /cqn2_6/ptodata/1/paa/US10_NEW_COMB.pep:US-10-037-667-4

seq_documentation_block:

```

; Sequence 4. Application US/10037667
; GENERAL INFORMATION:
; APPLICANT: Morgan, Bruce A.
; TITLE OF INVENTION: REGULATION OF NEURAL DEVELOPMENT BY
; TITLE OF INVENTION: DAEDALOS
; FILE REFERENCE: 10287-044001
; CURRENT APPLICATION NUMBER: US/10/037,667
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 60/243,110
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-037-667-4

```

alignment_scores:

```

Quality: 2458.50      Length: 518
Ratio: 4.947          Gaps: 5
Percent Similarity: 95.946      Percent Identity: 90.347

```

alignment_block:

us-08-711-417c-165.rapn

Wed Aug 28 10:05:41 2002

US-08-711-417C-165 x US-10-037-667-4

Align seg 1/1 to: US-10-037-667-4 from: 1 to: 515

```

1 ATGGATGCTCAGGAGGTCAAGACATGCTCTTCTCATCGAGGAGAAAG 50
1 MetAspValAspGluGlyGlnAspMetSerGlnValSerGlyLysGluSe 17
51 CCCCCTGTAGGCGATACCTCCAGATGAGGCGGATGAGCCCATCCGATCC 100
17 rProProValSerAspThrProAspGluGlyAspGluProMetProValP 34
101 CCGAGGACCTCTCCACACCTCGGAGGAGGAGAGAGAGAGAGAGAGAG 150
34 roGluAspLeuSerThrThrSerGlyAlaGlnGlnAsnSerLysSerAsp 50
151 AGAGTCGTGGCCAGCTAATGTAAGTAGAGACTCAGAGTGTATGAAGAG 200
51 ArgGlyMetAlaSerAsnValLysValGluThrGlnSerAspGluGluAs 67
201 TGGCGTGCCTGTGAAATGAATGGGAGGAATGTGCGGAGGATTTACGAA 250
67 nGlyArgAlaCysGluMetAsnGlyGluGluCysAlaGluAspLeuArgM 84
251 TGCTTGATGCTCGGAGAGAAATGAATGCTCCACAGGAGACCAAGGC 300
84 etLeuAspAlaSerGlyGluLysMetAsnGlySerHisArgAspGlnGly 100
301 AGCTCGGCTGTGCGGAGTGGAGGATTCGACTTCTTAAACGGAAAACT 350
101 SerSerAlaLeuSerGlyValGlyGlyLeuArgLeuProAsnGlyLysLe 117
351 AAAGTGTATATCTGTGGGATTCATTCGATCGGCGCCCAATGCTCATGG 400
117 uLysCysAspLeuGlyGlyLeuValCysIleGlyProAsnValLeuMetV 134
401 TTCACAAAGAGGACACACTCGAGAACGGCCCTTCCAGTGAATCAGTGC 450
134 alHisLysArgSerHisThrGlyGluArgProPheGlnCysAsnGlnCys 150
451 GGGGCTCATTCACCAAGGGAACCTGCTCGGACATCAAGCTGCA 500
151 GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuH 167
501 TTCGGGAGGAGCCCTTCAATGCCACTCTGCAACTACGCTCGCCGCC 550
167 sSerGlyGluLysProPheLysCysHisLeuCysAsnTyrAlaCysArg 184
551 GGAGGAGCCCTCACTGGCCACCTGAGAGCGCACTCGCTGGTAAACCT 600
184 rgArgAspAlaLeuThrGlyHisLeuArgThrHisSerValGlyLysPro 200
601 CACAATGTGGATATGTGGCGAAGCTATTAACAGCAAGCACTCTTTAGA 650
201 HisLysCysGlyTyrCysGlyArgSerTyrLysGlnArgSerSerLeuGl 217
651 GGAACATAAGAGCCGTCGCCAACAATCTTGGAAAGCATGGCCCTTCGG 700
217 uGluHisLysGluArgCysHisAsnTyrLeuGluSerMetGlyLeuPro 234
701 GCACACTGTACCCAGTCAATTAAGAGAACTAAGCAGCTGAATGCA 750
234 ly...ValCysProValIleLysGluGluThrAsnHisAsnGluMetAla 249
751 GAAGACCTGTGCAAGATAGGATCAGAGATCTCTCGTCTCGACAGACT 800
250 GluAspLeuCysLysIleGlyAlaGluArgSerLeuValLeuAspArgLe 266
801 AGCAAGTATGTGCGCAACGTAAGAGCTCTATGCTCAGAAATTTCTTG 850
266 uAlaSerAsnValAlaLysArgLysSerMetProGlnLysPheLeuG 283
851 GGGACAAAGGCCCTGTCCGACACGCCCTTACGACAGTGCACGAGAG 900

```

```

283 lyAspLysCysLeuSerAspMetProTyrAspSerAlaAsnTyrGluLys 299
901 GAGAACGAAATGATGAGTCCACGATGACCAAGCCATCAACAACGC 950
300 Glu...AspMetMetThrSerHisValMetAspGlnAlaIleAsnAl 315
951 CATCAACTACCTGGGGCGGAGTCCCTGCGCCGCTGGTGAGAGCCGCC 1000
315 alleAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrProp 332
1001 CGGCGGCTTCCAGAGTGTCCGCTCATCAGCCGATGATACCACTGCAC 1050
332 roGlySerSerGluValValProValIleSerSerMetTyrGlnLeuHis 348
1051 AGG...CGCTCGGAGGACCCCGCTCCCAACCACTCGGCCAGGACAG 1097
349 LysProProSerAspGlyProProArgSerAsnHisSerAlaGlnAsp 364
1098 CGCGCTGGAGTACCTGCTGCTCTCCAAGCCCAAGTTGTGCTCGCTCG 1147
365 .AlaValAspAsnLeuLeuLeuSerLysAlaLysSerValSerSerg 381
1148 AGCGGAGCGCTCCCGAGCAACACTGCCAAGACTCCACGACGACACCG 1197
381 luArgGluAlaSerProSerAsnSerCysGlnAspSerThrAspThrGlu 397
1198 AGCAACACAGGAGGAGCGGCTCTTATCTACCTGACCAACACACAT 1247
398 SerAsnAlaGluGluGlnArgSerGlyLeuIleTyrLeuThrAsnHisI 414
1248 CGCCCGACCGCGCAACGC...GTGCTGCTCAAGGAGGAGGACCGCGCT 1294
414 easnProHisAlaArgAsnGlyLeuAlaLeuLysGluGlnArgAlaI 431
1295 AGCACTGCTCGCGCGCTCGAGAACTCGAGGAGGAGGAGGAGGAGGAG 1344
431 yGluValLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArgVal 447
1345 GTCAGCACCGGCGGAGGAGAGTGAAGTGTACAGTGCAGACACTGCCG 1394
448 ValSerThrSerGlyGluGlnLeuLysValTyrLysCysGluHisCys 464
1395 GTGCTCTCTTCTGATCAGTACATGATGATGATGATGATGATGATGAT 1444
464 gValLeuPheLeuAspHisValMetTyrThrIleHisMetGlyCysHis 481
1445 GCTTCTGATCTCTTTTGTAGTGCAACATGTGCGGCTACCAAGGAGG 1494
481 lyPheArgAspProPheGluCysAsnMetCysGlyTyrHisSerGlnAsp 497
1495 CGGTACGAGTCTCGTGGACATACCGGAGGAGGAGGAGGAGGAGGAG 1544
498 ArgTyrGluPheSerSerHisIleThrArgGlyGluHisArgTyrHis 514
1545 GAGC 1548
514 user 515

```

seq_name: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-27

```

seq_documentation_block:
; Sequence 27, Application US/08733622C
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia
; APPLICANT: Morgan, Bruce A.
; TITLE OF INVENTION: AIOLOS GENE
; FILE REFERENCE: 10287-030001
; CURRENT APPLICATION NUMBER: US/08/733,622C
; PRIOR FILING DATE: 1996-10-17
; PRIOR APPLICATION NUMBER: US 60/017,646
; PRIOR FILING DATE: 1996-05-14
; PRIOR APPLICATION NUMBER: US 60/005,529

```

```
; PRIOR FILING DATE: 1995-10-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 518
; TYPE: PRM
; ORGANISM: Mus musculus
US-08-733-622C-27
```

alignment_scores:

```
Quality: 2437.00      Length: 521
Ratio: 4.913          Gaps: 6
Percent Similarity: 95.202 Percent Identity: 89.635
```

alignment_block:

```
US-08-711-417C-165 x US-08-733-622C-27 ..
```

```
Align seg 1/1 to: US-08-733-622C-27 from: 1 to: 518
```

```
1 ATGGATGCTGACGAGGTCACACATGCTTCTCATCAGGGAAGAAAG 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 MetAspValAspGluGlnAspMetSerGlnValSerGlyLysGluSe 17
51 CCCCCCTGTAAAGCATCTCCAGATGAGGGCGATGAGCCCATGCCGATCC 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 rProProValSerAspThrProAspGluGlyAspGluProMetProValp 34
101 CCGAGGACTCTCCACACCTCGGAGGACAGACAGCAAACTCCAGAGTGAC 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 roGluAspLeuSerThrThrSerGlyAlaGlnAsnSerLysSerAsp 50
151 AGAGTCGTGGCCAGTAATGTTAAAGTACAGACTCAGAGTATCATCAAGAGAA 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 ArgGlyMetAlaSerAsnValLysValGluThrGlnSerAspGluGluas 67
201 TGGCGTGCCTGTCAAATGATGGGGAAGAAATGTGCGGAGATTATACGAA 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67 nGlyArgAlaCysGluMetAsnGlyGluGluCysAlaGluAspLeuArgm 84
251 TGCTGTATGTCCTGGGAGAGAAATGAATGCCTCCACAGGAGACCAAGGC 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84 etLeuAspAlaSerGlyGluLysMetAsnGlySerHisArgAspGlnGly 100
301 AGCTCGCTTTCGCGGAGTTGAGGAGATTCGACTTCCTTAACGGAAACT 350
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101 SerSerAlaLeuSerGlyValGlyGlyIleArgLeuProAsnGlyLysLe 117
351 AAAGTGTGATATCTGTGGGATCATTTGTCATCGGCGCCCATGTGCTCATGG 400
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
117 ulysCysAspIleCysGlyIleValCysIleGlyProAsnValLeuMetV 134
401 TTCACAAAGAACCCACTGGAGAACGCCCTTCCAGTGAATCAATGTC 450
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
134 alHisLysArgSerHisThrGlyGluArgProPheGlnCysAsnGlnSer 150
451 GGGGCTCTATTACCCAGAGGCACTGCTCCCGGCACATCAAGCTGCA 500
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
151 GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHi 167
501 TTCGGGGAGAGCCCTTCAATGTCACCTCTGCAACTACCGCTGCCGCC 550
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
167 sSerGlyGluLysProPheLysCysHisLeuCysAsnTyrAlaCysArgA 184
551 GGAGGACCCCTCACTGGCCACCTGAGGAGCGACTCGGTTGGTAAACCT 600
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
184 rArgAspAlaLeuThrGlyHisLeuArgThrHisSerValGlyLysPro 200
601 CACAAATGTGGATATTGGCGGAGCTATAACACAGCAACGCTTTTAGA 650
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
201 HisLysCysGlyTyrCysGlyArgSerTyrLysGlnArgSerSerLeuG1 217
651 GGAACATAAGAGCGCTCCCAACAACACTACTTGGAAAGCATGGGCTTCCGG 700
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
217 uGluHisLysGluArgCysHisAsnTyrLeuGluSerMetGlyLeuProG 234
701 GCACACTGTACCCAGTCATTAAAGAGAACTAAGCAGCAGTGAATGCCA 750
|| :||:|||||:|||||:|||||:|||||:|||||:|||||
234 ly...ValCysProValIleLysGluThrAsnHisAsnGluMetAla 249
751 GAAGACCTGTGCAAGATAGGATCAGAGAGATCTCTCGCTGGACAGACT 800
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
250 GluAspLeuCysLysIleGlyAlaGluArgSerLeuValLeuAspArgLe 266
801 AGCAAGTAATGTCGCAACAGTAAGAGCTCTATGCTCAGAAATTTCTTG 850
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
266 uAlaSerAsnValAlaLysArgLysSerMetProGlnLysPheLeuG 283
851 GGGACAAGGGCCTGTCCGACAGCCCTACGACAGTGCACCTACGAGAAG 900
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
283 lyAspLysCysLeuSerAspMetProTyrAspSerAlaAsnTyrGluLys 299
901 GAGAAGCAATGATGAGTCCAGCTCCCTGCGCCCTGCTGTCAGACGCGCC 950
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
300 Glu...AspMetMetThrSerHisValMetAspGlnAlaIleAsnAsnAl 315
951 CATCAACTACCTGGGGCGGAGTCCCTGCGCCCTGCTGTCAGACGCGCC 1000
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
315 alIleAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrProp 332
1001 CGGCGGTTCAGAGTGGTCCCGCTCATCAGCCGATGTACCAAGTCCAG 1050
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
332 roGlySerSerGluValValProValIleSerSerMetTyrGlnLeuHis 348
1051 AGG...CGCTCGAGGAGCAGCCGCTCCCAACCACTCGGCCCGCAGCAG 1097
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
349 LysProProSerAspGlyProProArgSerAsnHisSerAlaGlnAsp.. 364
1098 CGCGCTGGAGTACCTGCTGCTCTCTCCAAAGCCAAAGTTGGTCCCTCG 1147
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
365 .AlaValAspAsnLeuLeuLeuSerLysAlaLysSerValSerSerG 381
1148 AGCGGAGGGTCCCGCAGCAGCAGCTGCTTATCTACCTGACCAACACAT 1197
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
381 LuArgGluAlaSerProSerAsnSerCysGlnAspSerThrAspThrGlu 397
1198 AGCAACACGAGGAGCAGCGCGCTCTTATCTACCTGACCAACACAT 1247
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
398 SerAsnAlaGluGluGlnArgSerGlyLeuIleTyrLeuThrAsnHisI 414
1248 CGCCCGCAGCGCGCAACGC...GTGTCGCTCAAGGAGGAGCAGCGCGCT 1294
| :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
414 eAsnProHisAlaArgAsnGlyLeuAlaLeuLysGluGluGlnArgAla 431
1295 AGACCTGCTGCGCGCGCTCCGAGAACTCGCAGAGCGCTCCGCGCTG 1344
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
431 yrGluValLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArgVal 447
1345 GTCAGCAGCAGCGCGGAGCAGATGAAGTGTACAAAGTGCAGAACACTGCCG 1394
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
448 ValSerThrSerGlyGluGlnLeuLysValTyrLysCysGluHisCysAr 464
1395 GGTGCTCTTCTCGATCAGCTCATGTACACCATCCACATG.....G 1435
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
464 gValLeuPheLeuAspHisValMetTyrThrIleHisMetGlyCysHisG 481
1436 GCTGCCAGCGCTTCCGTGATCTTTAGTGCACATGTGCGGCTACAC 1485
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
481 lyCysHisGlyPheArgAspProPheGluCysAsnMetCysGlyTyrHis 497
1486 AGCCAGGACCGGTACGAGTCTCTCTCCACATACCGGAGGAGGAGCAGCG 1535
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
498 SerGlnAspArgTyrGluPheSerSerHisIleThrArgGlyGluHisAr 514
1536 CTTCCACATGAGC 1548
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
```

us-08-711-417c-165.rapn

Wed Aug 28 10:05:41 2002

514 gTyrHisLeuSer 518

seq_name: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pap:US-08-733-622C-22

```

seq_documentation_block:
; Sequence 22, Application US/08733622C
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia
; APPLICANT: Morgan, Bruce A.
; TITLE OF INVENTION: AIOLOS GENE
; FILE REFERENCE: 10287-030001
; CURRENT APPLICATION NUMBER: US/08/733,622C
; CURRENT FILING DATE: 1996-10-17
; PRIOR APPLICATION NUMBER: US 60/017,646
; PRIOR FILING DATE: 1996-05-14
; PRIOR APPLICATION NUMBER: US 60/005,529
; PRIOR FILING DATE: 1995-10-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: majority sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(470)
; OTHER INFORMATION: Xaa - Any Amino Acid
US-08-733-622C-22

```

```

alignment_scores:
Quality: 2207.50      Length: 468
Ratio: 5.098          Gaps: 3
Percent Similarity: 92.521 Percent Identity: 90.385

```

alignment_block:

US-08-711-417C-165 x US-08-733-622C-22 ..

Align seg 1/1 to: US-08-733-622C-22 from: 1 to: 470

```

160 GCCAGTAAATGTTAAAGTAGAGACTCAGAGTGAAGAGAAATGGCGTGC 209
|||||
3 AlaSerAsnValLysValGluThrGlnSerAspGluAsnGlyArgAl 19
|||||
210 CTGTGAATGAATGGGAAGATGTCGGAGGATTTACGATGCTTGATG 259
|||||
19 acysGluMetAsnGlyGluGluCysAlaGluAspLeuArgMetLeuAspA 36
|||||
260 CCTCGGAGAGAAATGAATGCTCCACAGGACCAAGGACGCTCGGCT 309
|||||
36 laSerGlyGluLysMetAsnGlySerHisArgAspGlnGlySerSerAla 52
|||||
310 TTGTGCGGAGTGGAGGATTCGACTTCCTAACGGAAAATGAAGTGTA 359
|||||
53 LeuSerGlyValGlyGlyLeuArgLeuProAsnGlyLysLeuLysCysAs 69
|||||
360 TATCTGTGGGATCATTTGCATCGGCGCCCAATGCTCATGTTTACAAAA 409
|||||
69 pileCysGlyIle***CysIleGlyProAsnValLeuMetValHisLysA 86
|||||
410 GAAGCCACACTGAGAACGGCCCTTCCAGTGCATCATAGTGGCGGCGCTCA 459
|||||
86 rGserHisThrGlyGluArgProPheGlnCysAsnGlnCysGlyAlaSer 102
|||||
460 TTCACCCAGAGGCAACCTGCTCGGACATCAAGCTGCAATTCGGGGA 509
|||||
103 PheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHisSerGlyGl 119
|||||
510 GAAGCCCTTCAATGCGACCTCTGCAACTACGCTGCGCGCGGAGGAGC 559
|||||
119 uLysProPheLysCysHisLeuCysAsnTyrAlaCysArgArgAspA 136

```

```

560 CCTCACTGCCACCTGAGAGCGCACTCGTGGTAAACCTCACAATGT 609
|||||
136 laLeuThrGlyHisLeuArgThrHisSerValGlyLysProHisLysCys 152
|||||
610 GGATATTGTGGCGGAGAGCTATAAACACAGCGAAGCTTTTAGAGAGACATAA 659
|||||
153 GlyTyrCysGlyArgSerTyrLysGlnArg***SerLeuGluGluHisLys 169
|||||
660 AGAGCGCTGCCACAACTACTGTGAAACCATGGCCCTTCGGGGCACACTGT 709
|||||
169 sgluArgCysHisAsnTyrLeuGluSerMetGlyLeuProGly***** 186
|||||
710 ACCAGTCAATTAAGAGAACTAAGCACAGTGAATGCGAGAACCTG 759
|||||
186 **ProValIleLysGluGluThr***His**GluMetAlaGluAspLeu 202
|||||
760 TGCAAGATAGATGAGAGATCTCTCGTGTGGACAGACTAGCAAGTAA 809
|||||
203 CysLysIleGly***GluArgSerLeuValLeuAspArgLeuAlaSerAs 219
|||||
810 TGTCGCCAAAGCTAAGAGCTCTATGCTCTCAAGAAATTTCTTGGGACAAG 859
|||||
219 nValAlaLysArgLysSerSerMetProGlnLysPheLeuGlyAspLys* 236
|||||
860 GCCTGTCCGACACGCGCTACGACAGTGCACGTCAGAGAGGAGAACGAA 909
|||||
236 **LeuSerAsp**ProTyrAspSerAla***TyrGluLysGlu***** 252
|||||
910 ATGATGAAGTCCAGCTGATGACCAAGCCATCAACACGCGCATCAACTA 959
|||||
253 MetMet***SerHisValMetAsp***AlaIleAsnAlaIleAsnTy 269
|||||
960 CQTGGGGCGGAGTCCCTGCGCCCTGCTGTCAGAGAGCGCCCGCGGTT 1009
|||||
269 rLeuGlyAlaGluSerLeuArgProLeuValGlnThrProProGly***S 286
|||||
1010 CCGAGTGTGTCGGGTCAACGCGGATGTCAGCTGCAC...AGGCGC 1036
|||||
286 erGluValValProValIleSerProMetTyrGlnLeuHis***** 302
|||||
1057 TCAGAGGCGCACCCCGCGCTCCAAACACTCGGCCAGGACGCGCGCTGA 1106
|||||
303 Ser***Gly***ProArgSerAsnHisSerAlaGlnAsp***AlaVal** 319
|||||
1107 GTACCTGCTCTCTCTCCAAAGCCAAAGTGTGTCCTCGAGCGCGAGG 1156
|||||
319 ***LeuLeuLeuLeuSerLysLysLys***Val***SerGluArgGluA 336
|||||
1157 CGTCCCGGAGCAACAGCTGCCAAGACTCCACGAGACACCGAGAGCAACAC 1206
|||||
336 laSerProSerAsnSerCysGlnAspSerThrAspThrGluSerAsn*** 352
|||||
1207 GAGGAGAGCGCAGCGGTCTTATCTACCTGACCAACACATCGCCGAGC 1256
|||||
353 GluGluGlnArgSerGlyLeuIleTyrLeuThrAsnHisIle***** 369
|||||
1257 CGCG...CAACGCGTGTCTGCTCAAGGAGGAGCACCGCGCTACGACCTGC 1303
|||||
369 *Ala*****LeuLysGluGlu***ArgAlaTyr*****L 386
|||||
1304 TCGCGCGCGCTCCGAGAACTCGCAGACGCGCTCCGCGTGTGACGACC 1353
|||||
386 euArgAlaAlaSerGluAsnSerGlnAspAla***ArgValValSerThr 402
|||||
1354 ACCGGGGAGAGATGAAGTGTACAAGTGCAGAACACTGCGCGGTGCTCTT 1403
|||||
403 SerGlyGluGln***LysValTyrLysCysGluHisCysArgValLeuPh 419
|||||
1404 CQTGGATCAGCTCATGTATACCATCCACATG.....GGTGGCCAGC 1444
|||||
419 eLeuAspHisValMetTyrThrIleHisMet*****GlyCysHisG 436

```


1445 GCTTCGGATGCTCTTTCAGTGCACAACTGTCGGCTACCAAGCCAGGAC 1494
436 lyphEARASppropheGluCysasnMetCysGlyTyrHisSerGlnAsp 452
1495 CGGTACGAGTTCCTCGTCGCACATAACGCGAGGGAGCAGCCGCTTCACAT 1544
453 ArgTyrGluPheSerSerHisIleThrArgGlyGluHisArg***His** 469
1545 GAGC 1548
469 *Ser 470

seq_name: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-26

seq_documentation_block:

; Sequence 26, Application US/08733622C

GENERAL INFORMATION:

APPLICANT: Georgopoulos, Katia

APPLICANT: Morgan, Bruce A.

; TITLE OF INVENTION: AIOLOS GENE

; FILE REFERENCE: 10287-030001

; CURRENT APPLICATION NUMBER: US/08/733,622C

; CURRENT FILING DATE: 1996-10-

; PRIOR APPLICATION NUMBER: US 60/017,646

; PRIOR FILING DATE: 1996-05-14

; PRIOR APPLICATION NUMBER: US 60/005,529

; PRIOR FILING DATE: 1995-10-18

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: Fas

; SEQ ID NO 26

; LENGTH: 4

```

; TYPE: PRT

```

; ORGANISM: Mus

alignment_scores:

Quality:	1963.00	Length:	521
----------	---------	---------	-----

Ratio: 4.776

Percent Similarity:	78.887	Percent Identity:	74.280
Percent Similarity:	78.887	Percent Identity:	74.280

alignment_block:

US-08-711-417C-165 x US-08-733-622C-26

Align seg 1/1 to: US-08-733-622C-26 from: 1 to: 432

1 ATGGATGCTGACGAGGGTCAAGACATGTCTTTTCTCATCCCAACCCAC

|||||:|||||

1 MetAspValAspGluGlyGlnAspMetSerGlnValSerGlyIysGlnGlu

1. 1980-1981

51 CCCCCCTGTAAGCGATACTCCAGATGAGGGCGATGAGCCCCATGCCCGATCC 100

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

17 rProValSerAspThrProAspGluGlyAspGluProMetProValp 34

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

101 CCGAGGACCTCTCCACCACCTCGGGAGGACAGCAAGCTCCAAGAGTGAC 150

[illegible]

34 roGluAspLeuSerThrThrSerGlyAlaGlnGlnAsnSerLysSerAsp 50

[illegible]

151 AGAGTCGTGGCCAGTAATGTTAAAGTAGAGACTCAGAGTGAAGAGAA 200

[illegible]

Wed Aug 28 10:05:41 2002

```

1248 CGCCGACGCGCGCAACGC...GTGTCGCTCAAGAGAGAGACGCGCGCT 1294
      |||:::
328 eAsnProHisAlaArgAsnGlyLeuAlaLeuLysGluGluGlnArgAla 345
1295 AGCACTGCTGCGCGCGCGCTCCGAGAACTCGCAGGACGCGCTCGCGGTG 1344
      |||:::
345 yGluValLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArgVal 361
1345 GTCAGCACGCGCGGAGCAGATGAAGTGTACAGTCCGCAACACTGCGCG 1394
      |||:::
362 ValSerThrSerGlyGluGlnLeuLysValTyrLysCysGluHisCysAr 378
1395 GTGCTCTTCCTGGATCAGCTCATGTACACCATCCACATG.....G 1435
      |||:::
378 gValLeuPheLeuAspHisValMetTyrThrIleHisMetGlyCysHisG 395
1436 GGTGCCACGCGCTTCGCTGATCCCTTTTGTAGTCAACATGTCGGGCTACCAC 1485
      |||:::
395 lCysHisGlyPheArgAspProPheGluCysAsnMetCysGlyTyrHis 411
1486 AGCAGGACCGGTACGAGTTCCTGTCGCACATAACGCGAGGCGGACCGG 1535
      |||:::
412 SerGlnAspArgTyrGluPheSerSerHisIleThrArgGlyGluHisAr 428
1536 CTCCACATGAGC 1548
      |||:::
428 gTyrHisLeuSer 432

```

seq_name: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pap:US-08-733-622C-24

seq_documentation_block:

; Sequence 24, Application US/08733622C

; GENERAL INFORMATION:

; APPLICANT: Georgopoulos, Katia

; APPLICANT: Morgan, Bruce A.

; TITLE OF INVENTION: AIOLOS GENE

; FILE REFERENCE: 10287-030001

; CURRENT APPLICATION NUMBER: US/08/733.622C

; CURRENT FILING DATE: 1996-10-17

; PRIOR APPLICATION NUMBER: US 60/017,646

; PRIOR FILING DATE: 1996-05-14

; PRIOR APPLICATION NUMBER: US 60/005,529

; PRIOR FILING DATE: 1995-10-18

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 24

; LENGTH: 431

; TYPE: PRT

; ORGANISM: Mus musculus

; US-08-733-622C-24

alignment_scores:

Quality: 1923.50 Length: 521

Ratio: 4.703 Gaps: 7

Percent Similarity: 78.503 Percent Identity: 73.129

alignment_block:

US-08-711-417C-165 x US-08-733-622C-24 ..

Align seg 1/1 to: US-08-733-622C-24 from: 1 to: 431

```

1 ATGGATGCTGACGAGGCTCAAGACATGCTTCTCATCAGGAGAAAG 50
      |||:::
1 MetAspValAspGluGlyGlnAspMetSerGlnValSerGlyLysGluSe 17
51 CCCCCCTGTAAGCGATCTCCAGATGAGGCGATGACCCCATGCCGATCC 100
      |||:::
17 rProProValSerAspThrProAspGluGlyAspGluProMetProValP 34
101 CCGAGGACCTCTCCACACCTCGGAGGACAGCAAGACTCCAAGAGTGAC 150
      |||:::
34 roGluAspLeuSerThrThrSerGlyAlaGlnGlnAsnSerLysSerAsp 50

```

```

151 AGAGTCGTGCCAGTAATGTTAAAGTAGAGACTCAGAGTGAAGAGAA 200
      |||:::
51 ArgGlyMet..... 53
201 TGGCGCTGCTGTGAAATGAATGGGGAAGAATGTGGGAGGATTTACGAA 250
      |||:::
53 ..... 53
251 TGCTTGATGCTCGGGAGAGAGAAATGAATGGCTCCACAGGAGCAAGGC 300
      |||:::
53 ..... 53
301 AGCTCGGCTTTGTGGGAGTTGGAGGCATTTCGACTTCCTAACGGAAACT 350
      |||:::
53 ..... 53
351 AAAGTGTGATATCTGGGATCAATTTGTCATCGGGCCCAATGTCTCATGG 400
      |||:::
53 ..... 53
401 TTCACAAAAGAGCCACACTGGAGACGGCCCTTCCAGTGCATCAATCAGTGC 450
      |||:::
54 .....GlyGluArgProPheGlnCysAsnGlnSer 63
451 GGGCCTCATTCACCCAGAGAGGCAACCTGCTCCGGCACATCAAGCTGCA 500
      |||:::
64 GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHi 80
501 TTCCGGGAGAGCCCTCAAAATGCCACCTCTGCAACTAGCCCTGCGGCC 550
      |||:::
80 sSerGlyGluLysProPheLysCysHisLeuCysAsnTyrAlaCysArgA 97
551 GGAGGACGCGCTCCTCAGTGGCCACCTGAGGACGCACTCCGTTGGTAAACCT 600
      |||:::
97 rArgAspAlaLeuThrGlyHisLeuArgThrHisSerValGlyLysPro 113
601 CACAAAATGTGATATTTGGCCGAGCTATAAACAGCAAGCTCTTTAGA 650
      |||:::
114 HisLysCysGlyTyrCysGlyArgSerTyrLysGlnArgSerSerLeuGl 130
651 GGAACATAAAGAGCGCTGCCACAACTACTTTGAAAGCATGGGCTTCGG 700
      |||:::
130 uGluHisLysGluArgCysHisAsnTyrLeuGluSerMetGlyLeuProG 147
701 GCACACTGCTACCGAGTCTATTAAAGAAAGCAAGTGAATGCA 750
      |||:::
147 lY...ValCysProValIleLysGluGluThrAsnHisAsnGluMetAla 162
751 GAAGACCTGTCAAGATAGGATCAGAGATCTCTCGTGTGGACAGACT 800
      |||:::
163 GluAspLeuCysLysIleGlyAlaGluArgSerLeuValLeuAspArgLe 179
801 AGCAAGTAATGTGCCAAACGTAAGAGCTCTATGCCTCAGAAATTTCTTG 850
      |||:::
179 uAlaSerAsnValAlaLysArgLysSerSerMetProGlnLysPheLeuG 196
851 GGGACAAGGCGCTGTCCGACAGCGCCCTACGAGTCCACCTACGAGAG 900
      |||:::
196 lYAspLysCysLeuSerAspMetProTyrAspSerAlaAsnTyrGluLys 212
901 GAGAAGCAAAATGATGAAGTCCACGCTGATGGACCAAGCCATCAACAACGC 950
      |||:::
213 Glu...AspMetMetThrSerHisValMetAspGlnAlaIleAsnAla 228
951 CATCAACTACCTGGGGCGGAGTCCCTGCGCGCTGCGGAGGAGCGGCC 1000
      |||:::
228 aIleAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrProP 245
1001 CCGGGGTTCCAGAGTGGTCCCGGTCATCAGCCCGATGTACCAGCTGCAC 1050
      |||:::
245 roGlySerSerGluValValProValIleSerSerMetTyrGlnLeuHis 261

```



```

1051 AGG...CGTCGGAGGAGCCGCCGCTCCAAACCACTCGGCCAGACAG 1097
::: |||:|||| |||:|||| |||:|||| |||:|||| |||:||||
262 LysProSerAspGlyProProArgSerAsnHisSerAlaGlnAsp... 277
1098 CGCCGTGGAGTACCTGCTGCTCTCCAGGCCAAGTTGTGCCCTCGG 1147
||||:|||| |||:|||| |||:|||| |||:|||| |||:||||
278 .AlaValAspAsnLeuLeuLeuSerLysAlaLysSerValSerSerg 294
1148 AGGCCAGGCGTCCCGAGCAACAGCTGCCAAGACTCCACGGACACCGAG 1197
||||:|||| |||:|||| |||:|||| |||:|||| |||:||||
294 LuArgGluAlaSerProSerAsnSerCysGlnAspSerThrAspThrGlu 310
1198 AGCAACAACAGGAGAGCGCGAGCGGTCTTATCTACCTGACCAACACAT 1247
||||:|||| |||:|||| |||:|||| |||:|||| |||:||||
311 SerAsnAlaGluGluGlnArgSerGlyLeuIleTyrLeuThrAsnHisI 327
1248 CGCCCGACGCGCGCAACGC...GTGTCGCTCAAGGAGGAGACCGCGCT 1294
| :||:||||: |||:||||: |||:||||: |||:||||: |||:||||
327 eAsnProHisAlaArgAsnGlyLeuAlaLeuLysGluGlnArgAlaT 344
1295 AGACCTGCTGCGCGCGCTCCGAACTCCGAGACGCGCTCCGCGTG 1344
||:||||: |||:||||: |||:||||: |||:||||: |||:||||
344 yrGluValLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArgVal 360
1345 GTCAGACAGCGGGAGAGAGTACAGGTACAGTGCAGAACACTGCCG 1394
||||:|||| |||:|||| |||:|||| |||:|||| |||:||||
361 ValSerThrSerGlyGluGlnLeuLysValTyrLysCysGluHisCysAr 377
1395 GGTGCTCTTCCTGGATCAGTGTACACCATCCACATG.....G 1435
||||:|||| |||:|||| |||:|||| |||:|||| |||:||||
377 gValLeuPheLeuAspHisValMetTyrThrIleHisMetGlyCysHisG 394
1436 GCTGCCAGCGCTTCCTGATCTCTTTAGTGCAACATGTGCGGCTACCAC 1485
||||:|||| |||:|||| |||:|||| |||:|||| |||:||||
394 LysCysHisGlyPheArgAspProPheGluCysAsnMetCysGlyTyrHis 410
1486 AGCCAGGCGGTACAGTCTCGTCGCGACATAACGCCGAGGGAGACGG 1535
||||:|||| |||:|||| |||:|||| |||:|||| |||:||||
411 SerGlnAspArgTyrGluPheSerSerHisIleThrArgGlyGluHisAr 427
1536 CTTCACATGAGC 1548
||:||||: |||
427 gTyrHisLeuSer 431

```

seq_name: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-23

seq_documentation_block:

; Sequence 23, Application us/08733622C

; GENERAL INFORMATION:

; APPLICANT: Georgopoulos, Katia

; TITLE OF INVENTION: AIOLOS GENE

; FILE REFERENCE: 10287-030001

; CURRENT APPLICATION NUMBER: US/08/733,622C

; CURRENT FILING DATE: 1996-10-17

; PRIOR APPLICATION NUMBER: US 60/017,646

; PRIOR FILING DATE: 1996-05-14

; PRIOR APPLICATION NUMBER: US 60/005,529

; PRIOR FILING DATE: 1995-10-18

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 23

; LENGTH: 334

; TYPE: PRT

; ORGANISM: Homo sapiens

US-08-733-622C-23

alignment_scores:

Quality: 1740.00

Ratio: 5.210

Percent Similarity: 88.830

Length: 376

Gaps: 1

Percent Identity: 88.830

```

alignment_block:
US-08-711-417C-165 x US-08-733-622C-23
Align seg 1/1 to: US-08-733-622C-23 from: 1 to: 334

421 GGAGAACGGCCCTTCCAGTGAATCACTGGGGCCCTCATTCACCCAGAA 470
1 GlyGluArgProPheGlnCysAsnGlnCysGlyAlaSerPheThrGlnLy 17
471 GGGCAACCTGCTCCGGCAGCATCAAGCTGCATTCCGGGAGAGCCCTTCA 520
17 sGlyAsnLeuLeuArgHisIleLysLeuHisSerGlyGluLysProPheL 34
521 AATCCACCTCTGCAACTAGCCCTGCCCGGGAGGAGCGCCCTCACTGGC 570
34 ysCysHisLeuCysAsnTyrAlaCysArgArgArgAspAlaLeuThrGly 50
571 CACTGAGGAGGCACTCGTGTGTTAAACCTCACAATGTGGATATTGTGG 620
51 HisLeuArgThrHisSer..... 56
621 CCGAAGCTATATAACAGCGAAGCTCTTTAGAGAAACATAAAGAGCGCTGC 670
56 ..... 56
671 ACAACTACTTGGAAAGCATGGGCTTCGGGGCACACTGTACCCAGTCATT 720
57 .....Valile 58
721 AAAGAAGAAATAAGCACAGTGAATGGCAGAGACCTGTGCAAGATAGG 770
59 LysGluGluThrLysHisSerGluMetAlaGluLeuLeuLysCysLysIleGl 75
771 ATCAGAGAGATCTCTCGTGTGGACAGACTAGCAAGTAATGTCGCCAAC 820
75 ySerGluArgSerLeuValLeuAspArgLeuAlaSerAsnValAlaLysA 92
821 GTAAGAGCTCTATGCTCAGAAATTTCTTGGGACAAAGGGCTCTCCGAC 870
92 rGlySerSerMetProGlnLysPheLeuGlyAspLysGlyLeuSerAsp 108
871 ACGCCTACGACAGTGCACGTACGAGAGGAGAAACGAAATGATGAAGTC 920
109 ThrProLysAspSerAlaThrTyrGluLysGluAsnGluMetMetLysSe 125
921 CCAGTGATGGACCAAGCCATCAACACGCCATCACTACCTGGGGCCCG 970
125 rHisValMetAspGlnAlaIleAsnAsnAlaIleAsnTyrLeuGlyAlaG 142
971 AGTCCTGCGCCGCTGCTGTCAGAGCGCCCGGGGGTTCGGAGGTGTC 1020
142 LuSerLeuArgProLeuValGlnThrProProGlyGlySerGluValVal 158
1021 CCGGTCTATCAGCCCGATGTACACGTGCACAGCGCTCGGAGGCGACCCC 1070
159 ProValIleSerProMetTyrGlnLeuHisArgArgSerGluGlyThrPr 175
1071 CGGTCTCAACCACTCGGCGCCAGGACAGCGCGTGGAGTACCTGCTGCTGC 1120
175 oArgSerAsnHisSerAlaGlnAspSerAlaValIleTyrLeuLeuLeuL 192
1121 TCTCAAGGCCCAAGTTGTCCTCGGAGCGCGAGGGCTCCCGGAGCAAC 1170
192 euSerLysAlaLysLeuValProSerGluArgGluAlaSerProSerAsn 208
1171 AGCTGCCAAGACTCCACGGACACCGAGAGCAACACAGGAGGAGCGAGCAG 1220
209 SerCysGlnAspSerThrAspThrGluSerAsnAsnGluGluGlnArgSe 225
1221 CGGTCTTATCTACCTGACCAACACATCGCCCGGACGCGCGCAACGCTGT 1270
225 rGlyLeuIleTyrLeuThrAsnHisIleAlaArgArgAlaGlnArgValS 242

```

1271 CGCTCAAGGAGGACGCGCGCTACGACCTGCTGCGCGCCGCTCCGAG 1320
 |||||
 242 erLeuLysGluGluHisArgAlaTyrAspLeuLeuArgAlaLeuSerGlu 258
 |||||
 1321 AACTCGCAGGAGCGCTCCGCGTGGTCAGCACAGCGGGGAGCAGATGAA 1370
 |||||
 259 AsnSerGlnAspAlaLeuArgValSerThrSerGlyGluGlnMetLy 275
 |||||
 1371 GGTGTAAAGTGGAACTGCGCGGTGCTTCTCTGGATCAGTCATGT 1420
 |||||
 275 sValTyrLysCysGluHisCysArgValLeuPheLeuAspHisValMetT 292
 |||||
 1421 ACACCATCCACATGGCTGCGCAGGCTCCGTCGATCCCTTTGAGTGCAC 1470
 |||||
 292 yrThrIleHisMetGlyCysHisGlyPheArgAspProPheGluCysAsn 308
 |||||
 1471 ATGTGCGGTACACAGCAGGACGGTACGAGTTCTGTCGCACATAC 1520
 |||||
 309 MetCysGlyTyrHisSerGlnAspArgTyrGluPheSerSerHisIleth 325
 |||||
 1521 GCGAGGAGGACCGCTTCCACATGAGC 1548
 |||||
 325 rArgGlyGluHisArgPheHisMetSer 334
 |||||

seq_name: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:us-08-733-622C-28

seq_documentation_block:

; Sequence 28, Application US/08733622C
 ; GENERAL INFORMATION:
 ; APPLICANT: Georgopoulos, Katia
 ; APPLICANT: Morgan, Bruce A.
 ; TITLE OF INVENTION: AIOLOS GENE
 ; CURRENT APPLICATION NUMBER: US/08/733,622C
 ; CURRENT FILING DATE: 1996-10-17
 ; PRIOR APPLICATION NUMBER: US 60/017,646
 ; PRIOR FILING DATE: 1996-05-14
 ; PRIOR APPLICATION NUMBER: US 60/005,529
 ; PRIOR FILING DATE: 1995-10-18
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 28
 ; LENGTH: 390
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-08-733-622C-28

alignment_scores:

Quality: 1681.00 Length: 521
 Ratio: 4.556 Gaps: 7
 Percent Similarity: 70.825 Percent Identity: 65.835

alignment_block:

US-08-711-417C-165 x US-08-733-622C-28 ..

Align seg 1/1 to: US-08-733-622C-28 from: 1 to: 390

1 ATGATGCTGACGAGGCTCAAGACATGTCTTCTCATCAGGGAAGAAAG 50
 |||||
 1 MetAspValaspGluGlnAspMetSerGlnValSerGlyLysGluSe 17
 |||||
 51 CCCCCCTTAAGCATCTCCAGATGAGGGGATGAGCCCATGCCGATCC 100
 |||||
 17 rProProValSerAspThrProAspGluGlyAspGluProMetProValP 34
 |||||
 101 CCGAGGACCTCTCCACCTCGGAGGACACCAAGCTCCAAGATGAC 150
 |||||
 34 roGluAspLeuSerThrThrSerGlyAlaGlnGlnAsnSerLysSerAsp 50
 |||||
 151 AGAGTCGTGGCCCAAGTATGTTAAAGTAGAGACTCAGAGTGATGAAGAA 200
 |||||
 51 ArgGlyMet..... 53

201 TGGCGCTGCTGTGAATGAATGGGGAAGAATGTGCGGAGGATTTACGAA 250
 53 53
 251 TGCTTGATGCTCGGGAGAGAAAATGAATGGTCCCAACAGGACCAAGGC 300
 53 53
 301 AGCTCGGCTTTGTCGGGAGTTGGAGGACATTCGACTTCTTAACGGAAGAACT 350
 53 53
 351 AAAGTGTGATATCTGTGGGATCATTTTCATCGGGCCCAATGTGCTCATGG 400
 53 53
 401 TTCACAAAAGAACCCACACTGGAGAACGGCCCTTCCAGTGCATCAGTGC 450
 54GlyGluArgProPheGlnCysAsnGlnSer 63
 451 GGGGCCTCATTTACCCAGAGAGGCAACTGCTCCGGCACATCAAGCTGCA 500
 |||||
 64 GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuH 80
 |||||
 501 TTCGGGGAGAGCCCTTCAAAATGCCACCTCTGCACTACGCTGCGCGCC 550
 |||||
 80 sSerGlyGluLysProPheLysCysHisLeuCysAsnTyrAlaCysArgA 97
 |||||
 551 GGAGGAGCGCCCTCAGTGGCCACCTGAGGAGCGACATCCGTTGGTAAACCT 600
 |||||
 97 rGArgspAlaLeuThrGlyHisLeuArgThrHisSer..... 109
 601 CACAAATGTGGATATTGTGCGCGAAGCTATAAACAGCGACGCTTTTGA 650
 109 109
 651 GGAACATAAAGAGCGCTGCCACAACACTACTTGGAAAGCATGGGCTTCCGG 700
 109 109
 701 GCACACTGTACCCAGTCATTAAAGAGAACTAAGCACAGTGAATGGCA 750
 |||||
 110ValIleLysGluGluThrAsnHisAsnGluMetAla 121
 |||||
 751 GAAGACCTGTCAAGATAGGATCAGAGATCTCTGCTGCTGGACAGACT 800
 |||||
 122 GluAspLeuCysLysIleGlyAlaGluArgSerLeuValLeuAspArgLe 138
 |||||
 801 AGCAAGTAATGTGCGCCAAACGTAAAGACTCTATGCTCTAGAAATTTCTTG 850
 |||||
 138 uAlaSerAsnValAlaLysArgLysSerSerMetProGlnLysPheLeuG 155
 851 GGGACAAGGCGCTCTCCGACACGCCCTTACACAGTGCACGCTACGAGAG 900
 |||||
 155 LyAspLysCysLeuSerAspMetProTyrAspSerAlaAsnTyrGluLys 171
 |||||
 901 GAGAACGAAATGATGAAGTCCACGCTGATGGACCAAGCCATCAACACGC 950
 |||||
 172 Glu....AspMetMetThrSerHisValMetAspGlnAlaIleAsnAsnAl 187
 |||||
 951 CATCAACTACTTGGGGCCGAGTCCCTGCGCCCGCTGGTGGTCAGACGCCCC 1000
 |||||
 187 aIleAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrProp 204
 |||||
 1001 CCGCGGTTCCGAGGTGGTCCCGGTATCATGCGCCGCTGTACCAAGCTGCAC 1050
 |||||
 204 roGlySerSerGluValValProValIleSerSerMetTyrGlnLeuHis 220
 |||||
 1051 AGG...CGCTCGGAGGACCCCGCGCTCCAACTCGGCCCGCAGGACAG 1097
 |||||
 221 LysProProSerAspGlyProProArgSerAsnHisSerAlaGlnAsp.. 236

```
1098 CCCCCTGGAGTACCTGCTGCTCTCCAAAGGCCAAGTTGGTCCCTCGG 1147
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
237 AlaValAspAsnLeuLeuLeuLeuLeuLeuLysAlaLysSerValSerSerG 253
1148 AGCGGAGCGCTCCCGGAGCAACAGCTGCCAAGACTCCACGGACACCGAG 1197
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
253 LuArgLysSerProSerAsnSerCysGlnAspSerThrAspThrGlu 269
1198 AGCAACACGAGGAGCGCGGCTTTATCTACCTGACCAACACACAT 1247
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
270 SerAsnAlaGluGluGlnArgSerGlyLeuLeuLeuLeuLeuLeuLeuLeu 286
1248 CCCCAGCGCGGCAACGC...GTGTCCTCAAGAGGAGGACCGCGCT 1294
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
286 eAsnProHisAlaArgAsnGlyLeuAlaLeuLysGluGlnArgAla 303
1295 AGCACTCTCGCGCGCGCTCCGAGAACTCCAGGAGCGCTCCGGTG 1344
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
303 yGluValLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArgVal 319
1345 GTACGACCGCGGAGCAGAGTACAAAGTGTACAGTCCGAACACTGCCG 1394
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
320 ValSerThrSerGlyGluGlnLeuLysValTyrLysCysGluHisCysAr 336
1395 GTGTCTCTCTGGATCAGCTCATCTACACCATCCACATG.....G 1435
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
336 gValLeuPheLeuAspHisValMetTyrThrIleHisMetGlyCysHisG 353
1436 GCTGCGCGGCTTCCTGATCTCTTTAGTGCACATGTGGGCTACAC 1485
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
353 lYcysHisGlyPheArgaspProPheGluCysAsnMetCysGlyTyrHis 369
1486 AGCCAGGACCGGTACAGTTCGTGTCGACATACGCGAGGGGAGCACCG 1535
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
370 SerGlnAspArgTyrGluPheSerSerHisIleThrArgGlyGluHisAr 386
1536 CTTCCACATGACG 1548
386 gTyrHisLeuSer 390
```

seq_name: /cgn2_6/ptodata/1/pas/US08_NEW_COMB.pep:US-08-733-622C-29

```
seq_documentation_block:
; Sequence 29, Application US/08733622C
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia
; APPLICANT: Morgan, Bruce A.
; TITLE OF INVENTION: AIOLOS GENE
; FILE REFERENCE: 10287-030001
; CURRENT APPLICATION NUMBER: US/08/733,622C
; PRIOR FILING DATE: 1996-10-17
; PRIOR APPLICATION NUMBER: US 60/017,646
; PRIOR FILING DATE: 1996-05-14
; PRIOR APPLICATION NUMBER: US 60/005,529
; PRIOR FILING DATE: 1995-10-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-733-622C-29
```

alignment_scores:
Quality: 1625.00 Length: 521
Ratio: 4.565 Gaps: 6
Percent Similarity: 68.330 Percent Identity: 63.724

alignment_block:
US-08-711-417c-165 x US-08-733-622C-29 ..

Align seg 1/1 to: US-08-733-622C-29 from: 1 to: 376

```
1 ATGGATGCTGACGAGGCTCAAGACATGCTCTTTCTCATCAGGAGGAAG 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MetAspValAspGluGlnAspMetSerGlnValSerGlyLysGluSer 17
51 CCCCCCTGTAAAGCATACTCCAGATGAGGCGGATGAGCCCATGCCGATCC 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 rProProValSerAspThrProAspGluGlyAspGluProMetProValp 34
101 CCGAGGACCTCTCCACCACTCGGGAGGAGCAGCAAGCTCCCAAGAGTGAC 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 roGluAspLeuSerThrThrSerGlyAlaGlnGlnAsnSerLysSerAsp 50
151 AGAGTCGTGCCCAAGTAATGTTAAAGTAGAGACTCAGAGTGATGAAGAGAA 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 ArgGlyMetAlaSerAsnValLysValGluThrGlnSerAspGluGluAs 67
201 TGGCGCTGCTGTGAATGAATGGGAAGAATGTGCGGAGGATTTACGAA 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67 nGlyArgAlaCysGluMetAsnGlyGluGluCysAlaGluAspLeuArgM 84
251 TGCTTGATGCTCGGAGAGAGAAATGAATGGCTCCACAGGAGGACCAAGGC 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84 etLeuAspAlaSerGlyGluLysMetAsnGlySerHisArgaspGlnGly 100
301 AGCTCGGCTTTGTCGGAGTTGGAGGCATTTCGACTTCCTAAACGGAAGAACT 350
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
101 SerSerAlaLeuSerGlyValGlyGlyIleArgLeuProAsnGlyLysLe 117
351 AAAGTCGTGATATCTGGGATCATTTTCATCGGGCCCAATGTGCTCATGG 400
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
117 uLysCysaspIleCysGlyIleValCysIleGlyProAsnValLeuMetV 134
401 TTCACAAAAGACCACTGGAGAGCGGCCCTTCAGTGCATCAGTCAGTC 450
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
134 alHisLysArgSerHisThr..... 140
451 GGGGCTCATTCACCCAGAGGGCAACCTGCTCCGGCACATCAAGCTGCA 500
140 ..... 140
501 TTCGGGGGAGAGGCCCTTCAATGCCACCTCTGCAACTACGCTGCCGCC 550
140 ..... 140
551 GGAGGGAGCGCCCTCCTGCGCCACCTGAGGAGCAGCACTCCGTTGGTAACCT 600
140 ..... 140
601 CACAAATGTGGATATTGTGCGCGAAGCTATAAACACAGCGAAGCTTTTGA 650
140 ..... 140
651 GGAACATAAAGAGCGCTGCCACAACTACTTTGGAAAGCATGGGCTTCCGG 700
140 ..... 140
701 GCACACTGTACCCAGTCAATTAAGAAAGAACTAAGCACACATGAAATGGCA 750
140 ..... 140
751 GAAGACCTGTGCAAGATAGGATCAGAGAGATCTCTCGTGTGGACAGACT 800
140 ..... 140
801 AGCAAGTAATGTCGCCAAACGTAAGAGCTCTATGCCCTCAGAAATTTCTTG 850
141 ..... 141
851 GGGACAGGGCGCTGTCGACAGCGCCCTACGACAGTGCACAGTGCACGAGAAG 900
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
141 lYAspLysCysLeuSerAspMetProTyrAspSerAlaAsnTyrGluLys 157
```


[illegible]

```
seq_name: /cgn2_6/ptodata/1/paa/US08_NEW_COMB pep: US-08-733-622C-2
seq_documentation_block:
```

```

; Sequence 2, Application US/087333622C
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia
; APPLICANT: Morgan, Bruce A.
; TITLE OF INVENTION: AIOLOS GENE
; FILE REFERENCE: 10287-030001
; CURRENT APPLICATION NUMBER: US/08/733,622C
; CURRENT FILING DATE: 1996-10-17
; PRIOR APPLICATION NUMBER: US 60/017,646
; PRIOR FILING DATE: 1996-05-14
; PRIOR APPLICATION NUMBER: US 60/005,529
; PRIOR FILING DATE: 1995-10-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-733-622C-2

alignment_scores:
    Quality: 1302.00      Length: 526
    Ratio: 3.305          Gaps: 16
    Percent Similarity: 74.905    Percent Identity: 52.281

alignment_block:
US-08-711-417C-165 x US-08-733-622C-2

Align seg 1/1 to: US-08-733-622C-2 from: 1 to: 507

25  ATGCTCTTTCTCATCAGGAGGAAGCCCTCTTAAGCGATACTACGAG 74
      : : : : : : : : : : : : : : : : : : : : : : : :
8  ValGluLeuLysSerThrGluGluInProLeuProThrLusSerProAs 24
      : : : : : : : : : : : : : : : : : : : : : :
75  TCAG...GGCGATGAGCCATGCGCATGCCGAGGACCTCTCCACCACT 121
      : : : : : : : : : : : : : : : : : : : : : :
24  palaleuasnaspTyrSerLeuProLysProHisGluIleGluAsnVal 41
      : : : : : : : : : : : : : : : : : : : : : :
122 CGGGAGGACACAAAGCTCCAAAGAGTCACAGAGTCGTGGCCAGTAAT... 168
      : : : : : : : : : : : : : : : : : : : : : :
41  spSerArgGluAlaProalaasnGluaspluasplaglyGluasps 57
      : : : : : : : : : : : : : : : : : : : : : :
169  ....GTTAAAGTAGACTCAGAGTGATGAGAGAAATGGCGCTGCCGTG 212
      : : : : : : : : : : : : : : : : : : : : : :
58  MetLysValLysAspGluTyrSerAspArgAspGluAsnIleMetLys 74
      : : : : : : : : : : : : : : : : : : : : : :
213 TGAAGTAATGGGCAAGAATGTGCGGAGGATTTACGAATGCTTGATGCT 262
      : : : : : : : : : : : : : : : : : : : : : :
74  oGluPrometGly.....GGAGTTGGAGGCATTCCGACTCTCAA 81
      : : : : : : : : : : : : : : : : : : : : : :
263 CGGGAGAGAAATGAATGGTCTCCACAGGACCAAGCGACTCGGCTTTG 312
      : : : : : : : : : : : : : : : : : : : : : :
81  LuGluSerGluMetProTyrSerTyrAlaArgGluTyrSerAspTyrGlu 97
      : : : : : : : : : : : : : : : : : : : : : :
313 TCG.....GGAGTTGGAGGCATTCCGACTCTCAA 341
      : : : : : : : : : : : : : : : : : : : : : :
98  SerIleLysLeuGluArgHisValProTyrAspAsnSerArgProThr 114
      : : : : : : : : : : : : : : : : : : : : : :
342 CGGAAAACTAAAGTGTGATATCTGTGGGATCATTTCTCGGGCCCAATG 391
      : : : : : : : : : : : : : : : : : : : : : :
114 rGlyLysMetAsnCysAspValcysGlyLeuSerCysIleSerPheAsn 131
      : : : : : : : : : : : : : : : : : : : : : :
392 TGCTCATGTTTCACAAAAGAACCCACACGTGGAGAGCGGCCCTTCAGT 441
      : : : : : : : : : : : : : : : : : : : : : :
131  alLeuMetValHisLysArgSerHisThrGlyGluArgPropheGlnCys 147
      : : : : : : : : : : : : : : : : : : : : : :
442 AATCAGTGGCGGCGCTCATTCACCCAGAGGCGCAACCTGCTCCGCGCAT 491
      : : : : : : : : : : : : : : : : : : : : : :
148 AsnGlnCysGlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisI 164
      : : : : : : : : : : : : : : : : : : : : : :
492 CAAGCTGCATTCGGGGGAGAACGCCCTTCAATGCCACCTCTGCAACTAC 541
      : : : : : : : : : : : : : : : : : : : : : :

```

Wed Aug 28 10:05:41 2002

164 eLysLeuHisThrGlyGluLysProHehLysCysHisLeuCysAsnTyrA 181

542 CTCTCCGCGCGGAGGAGCGCCCTCACTGGCCACCTGAGGACGCACTCCGTT 591

181 lacysGlnArgArgAspAlaLeuThrGlyHisLeuArgThrHisSerVal 197

592 GGTAAACCTCACAATGTGGATATTGTGGCCCAAGCTATAAACAACGGAC 641

198 GluLysProTyrLysCysGluPheCysGlyArgSerTyrLysGlnArgSe 214

642 GTCTTTAGAGAAACATAAAGAGCGCTGCCACAACTACTTTGGAACGATGG 691

214 rSerLeuGluGluHisLysGluArgCysArgAlaPheLeuGlnAsnProA 231

692 GCCTTCGGGCGCACACTGTACCCAGTCATTAAAGACAGAAACTAAGCACACT 741

231 sPLeu...GlyAspAlaAlaSerVal.....GluAlaArgHisIle 243

742 GAAATGGCAGAAGACACCTGTGCAAGATAGGATCAGAGAGATCTCTCGTCT 791

244 Lys.....AlaGluMetGlySerGluArgAlaLeuValle 255

792 GGACAGACTAGCAAGTAATGTCCCAAAAGCTAAGAGCTCTATGCTCTCAGA 841

255 uAspArgLeuAlaSerAsnValAlaLysArgLysSerSerMetProGlnL 272

842 AATTTCTTGGGGCAAG...GGCCTGTGCCAGACGCCCTTACGACACTGCC 888

272 ysPheIleGlyGluLysArgHisCysPheAspAlaAsnTyrAsnProGly 288

889 ...ACGTACGAGAAGGAGAGAACGAATGATGAAGTCCCACTGATGAGACCA 935

289 TyrMetTyrGluLysGluAsnGluMetMetGlnThrArgMetMetAspGl 305

936 AGCCATCAACAAGCCCATCAACTACCTGGGGCGGAGTCCCTCGCGCCGC 985

305 nAlaIleAsnAlaIleSerTyrLeuGlyAlaGluAlaPheArgProL 322

986 TGGTGTACAGACCCCGCGGC...GGTTCGAGGTGTGCCGGTCTATCAGC 1032

322 euValGlnThrProProAlaProThrSerGluMetValProValIleSer 338

1033 CCGATGTACCAAGCTGCAC...AGGCGCTCGGAG.....GGCACCCC 1070

339 SerValTyrProIleAlaLeuThrArgAlaAspMetProMetGlyAlaPr 355

1071 GCGTGTCAACCACTCGGCCAGGACAGCGCGTGGAGTACTCTCTGCTGC 1120

355 oGlnGlu.....MetGluLysLysArgIleL 364

1121 TCTCCAAGGCCAAGTTGGTGCCTTCGAGGCGGAGCGTCCCGAGCAAC 1170

364 euLeuProGluLysIleLeuProSerGluArgGlyLeuSerProAsnAsn 380

1171 ACCTGCCAAGACTCCAGGACACCGAGCAACAACAGGAGGAGCAGCGCAG 1220

381 SerAlaGlnAspSerThrAspThrAspSerAsnHisGluAspArgGlnHi 397

1221 CGGTCTTTATCTACCTGACCAACCAACATC.....GCCGACGCGC 1258

397 s.....LeuTyrGlnGlnSerHisValValLeuProGlnAlaArgAsnG 412

1259 GCACACGGGTGTGCTTCAGGAGGAGGACACCGCGCTACGACCTCTCGTGGC 1308

412 lyMetProLeu...LeuLysGluValProArgSerPheGluLeuLeuLys 427

1309 GCGCGCTCCGAGAACTCCGACGAGCGCTCCGCGTGTGTACGACCAACGCG 1358

428 ProProProIleCysLeuArgAspSerIleLysValIleAsnLysGluGl 444

1359 GGACAGATGAAGGTGTACAAGTGGGAACACTGCCGGGTGTCTTCTCTGG 1408

444 yGluValMetAspValPheArgCysAspHisCysHisValLeuPheLeuA 461


```

342 CGGAAGAACTAAAGTGTATCTGGGATCATTTGCTCGGCGCCCAATG 391
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
114 rGlyLysMetMetCysAspValCysGlyLeuSerCysIleSerPheAsnV 131
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
392 TGCTCATGTGTTCAAAAGAACCCACACTGGAGAACGGCCCTTCCAGTGC 441
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
131 alLeuMetValHisLysArgSerHisThrGlyGluArgProPheGlnCys 147
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
442 AATCAGTGGGGGCTCTATTCACCCAGAGGCGCAACCTGTCGCGCACAT 491
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
148 AsnGlnCysGlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisI 164
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
492 CAAGCTGATTCCTCCGGGAGAGCCCTTCAATGCCACTCTGCAACTACG 541
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
164 elysLeuHisThrGlyGluLysProPheLysCysHisLeuCysAsnTyrA 181
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
542 CTGCGCGCGGAGGACCGCTCACTGGCCACCTGAGGAGCGCACTCGGTT 591
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
181 laCysGlnArgAspAlaLeuThrGlyHisLeuArgThrHisSerVal 197
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
592 GGTAAACCTCACAATGTGGATATTGTGGCCGAGCTATAAAGCAAGCAAC 641
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
198 GluLysProTyrLysCysGluPheCysGlyArgSerTyrLysGlnArgSe 214
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
642 GTCTTTAGAGCAATAAAGAGCGCTGCCACACTACTTCTGGAAAGCATGG 691
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
214 rSerLeuGluGluHisLysGluArgCysArgAlaPheLeuGlnAsnProA 231
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
692 CCTTCGCGGCGCACTGTACCCAGTCATTAAGAAAGAACTAAGCACAGT 741
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
231 spLeu...GlyAspAlaSerVal.....GluAlaArgHisIle 243
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
742 GAAATGCGCAGAACCTGTCCAGATAGATCAGAGAGATCTCTGCTGT 791
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
244 Lys.....AlaGluMetGlySerGluArgAlaLeuVal 255
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
792 GGACAGACTAGCAAGTAATGTCCCAACGTAAGAGCTCTATGCTCAGA 841
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
255 uAspArgLeuAlaSerAsnValAlaLysArgLysSerMetProGlnL 272
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
842 AATTCTCTGGGACAG...GGCTGTCTCGCACACCCCTAGCACAGTGC 888
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
272 ysPheIleGlyLysArgHisCysPheAspAlaAsnTyrAsnProGly 288
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
889 ...ACGTACGAGAAGAGAACCAATGATGAAGTCCACAGTGGACCA 935
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
289 TyrMetTyrGluLysGluAsnGluMetMetGlnThrArgMetMetAspG 305
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
936 AGCATCAACACAGCCATCACTACTGGGGCCGAGTCCCTGCGCGCGC 985
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
305 nAlaIleAsnAsnAlaIleSerTyrLeuGlyAlaGluAlaPheArgProL 322
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
986 TGGTGCAGACGCGCCCGGCG...GGTTCGAGGTGGTCCCGGTCATCAG 1032
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
322 euValGlnThrProAlaProThrSerGluMetValProValIleSer 338
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
1033 CGATGTACCACTGCAC...AGGCGCTCGGAG.....GGCACCCC 1070
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
339 SerValTyrProIleAlaLeuThrArgAlaAspMetProMetGlyAlaPr 355
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
1071 GCGTCCCAACCACTCGGCCAGGACCGCGCTGGAGTACCTCTGCTGC 1120
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
355 oGlnGlu.....MetGluLysLysArgIleL 364
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
1121 TCTCAGAGCCCAAGTTGGTCCCTCGGAGCGCGGAGCGTCCCGAGCAAC 1170
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
364 euLeuProGluLysIleLeuProSerGluArgGlyLeuSerProAsnAsn 380
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
1171 AGCTGCCAAGACTCCACGACCGAGCAACACAGGAGCAGCGCAG 1220
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
381 SerAlaGlnAspSerThrAspThrAspSerAsnHisGluAspArgGlnHi 397
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
1221 CGGTCTTATCTACCTGACCAACCACTC.....GCCCGACGG 1258
   :|||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:

```

```

seq_name: /cqn_6/ptodata/L/paa/US10_NEW_COMB.pap:US-10-037-667-1
seq_documentation_block:
; Sequence 1, Application US/10037667
; GENERAL INFORMATION:
; APPLICANT: Morgan, Bruce A.
; TITLE OF INVENTION: REGULATION OF NEURAL DEVELOPMENT BY
; FILE REFERENCE: 10287-044001
; CURRENT APPLICATION NUMBER: US/10/037, 667
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 60/243,110
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 537
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-037-667-1

```

alignment_scores:

```

Quality: 1282.50      Length: 532
Ratio: 3.402          Gaps: 16
Percent Similarity: 70.865      Percent Identity: 50.752

```

alignment_block:

```

US-08-711-417C-165 x US-10-037-667-1

```

```

Align seg 1/1 to: US-10-037-667-1 from: 1 to: 537

```

```

94 CCGATCCCGGAGGACCTCTCCACCACTCGGGAGGACAGCAAGCTCCAA 143
   |||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
22 ProValGlyProSerValSerThrProAsn...SerGlnHisSerSerPr 37
   |||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
144 GAGTGACAGAGTCTGGCCAGTAACTGTTAAAGTAGAGACTCAGAGTGATG 193
   |||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
37 oSerArgSerLeuSerAlaAsnSerIleLysValGluMetTyrSerAspG 54
   |||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
194 AAGAGATGGCGCTGCTGTGAATGAATGGGGAAGAATGTCGCGGAGGAT 243
   |||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
54 luGluSerSerArgLeu.....LeuGlyProasp 63
   |||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
244 TTACGAATGCTTCATCCCTCGGAGAGAAATG..... 276
   |||||:  |||||:  |||||:  |||||:  |||||:  |||||:  |||||:

```

Wed Aug 28 10:05:41 2002

```

64 GluArgLeuLeuAspLysAspSerValIleValGluAspSerLeuSe 80
277 .....AATGGCTCCACACAGGAGCAAGGACGCTCGG 307
80 rGluProLeuGlyTyrCysAspGlySerGlyProGluProHisSerPro. 96
308 CTTTGTGGGAGTGGAGGATTCGACTTCCTTAACGGAAACTAAAGT 357
97 .....GlyGlyIleArgLeuProAsnGlyLysLeuLysCys 108
358 GATATCTGGGATCATCTGCGGCGCAATGCTCATGTTTCACAA 407
109 AspValCysGlyMetValCysIleGlyProAsnValLeuMetValHisIly 125
408 AAGAAGCCACACTGGAGAGCGGCTTCAGTCGATCAGTCAGTCGGGCT 457
125 sArgSerHisThrGlyGluArgProPheHisCysAsnGlnCysGlyAlaAs 142
458 CATTCACCCAGAGGCAACCTCTCGGCACATCAAGCTGATTCGGG 507
142 erPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHisSerGly 158
508 GAGAAGCCCTTCAATGCCACTCTGCAACTAGCTGCGCGGAGGGA 557
159 GluLysProPheLysCysProPheCysAsnTyrAlaCysArgArgAs 175
558 GCGCTCTGACTGCGCACCTGAGGAGCGCACTCC.....GTTG 592
175 pAlaLeuThrGlyHisLeuLeuArgThrHisSerValSerProThrValG 192
593 GTAAACCTCACAAATGTGGATATTGTGCGCGCAACTATAACAGCAAG 642
192 LysProTyrLysCysAsnTyrCysGlyArgSerTyrLysGlnGlnSer 208
643 TCTTAGAGGAACATAAGAGCGCTGCCACAACTACTTGGAAACATG.. 690
209 ThrLeuGluGluHisLysGluArgCysHisAsnTyrLeuGlnSerLeuSe 225
691 .....GGCCTTCGCGGACACTGTACCCAGTCA 718
225 rThrAspAlaGlnAlaLeuThrGlyGlnProGly..... 236
719 TTAAGAGAACTAGCACAGTGAATGCGAGAGAC...CTGTGCAAG 765
237 .....AspGluIleArgAspLeuGluMetValProAspSerMetLeuHis 251
766 ATAGGATCAGAGAGATCTCTGCTGGGAGACACTAGCAAGTAATGTCGC 815
252 ProSerThrGluArgProThrPheIleAspArgLeuAlaAsnSerLeuTh 268
816 CAACAGTAAAGAGCTCTATGCTCAGAAATTTCTTGGGAGCAAG..... 858
268 rLysArgLysArgSerThrProGlnLysPheValGlyLysGlnMetA 285
859 .....GCCTGTCCGACACCGCTTACGAC.....AGTCCACGTAC 894
285 rgPheSerLeuSerAspLeuProTyrAspValAsnAlaSerGlyGlyTyr 301
895 GAGAGAGAGAGCAAAATGATGAGTCCCGCTGATGGACCAAGCCATCAA 944
302 GluLysAspValGluLeuValAlaHisHisGlyLeuGluProGlyPheG 318
945 CAACGCCATCAACTACTGCGGCGGAGTCCCTGCGCGCTGCTGCAGAG 994
318 yGlySerLeuAlaPheValGlyThrGluHisLeuArgProLeu...ArgL 334
995 CGCCCCCGGGCGGT.....TCCAGGTGTCCCGGTTCATCAGCCCGATG 1038
334 euProProThrAsnCysLysSerGluLeuThrProValIleSerSerVal 350
1039 TAC.....CAGCTGCACAGCGGCTCGGAG.....GCCACCCC 1070
351 TyrThrGlnMetGlnProIleProSerArgLeuGluLeuProGlySerAr

```

```

seq_name: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pap:US-10-037-667-5
seq_documentation_block:
; Sequence 5, Application US/10037667
; GENERAL INFORMATION:
; APPLICANT: Morgan, Bruce A.
; TITLE OF INVENTION: REGULATION OF NEURAL DEVELOPMENT BY
; FILE OF INVENTION: DAEDALOS
; FILE REFERENCE: 10287-044001
; CURRENT APPLICATION NUMBER: US/10/037,667
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 60/243,110
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-037-667-5

alignment_scores:
Quality: 1126.00      Length: 546
Ratio: 3.283          Gaps: 17
Percent Similarity: 62.821      Percent Identity: 44.322

alignment_block:
US-08-711-417c-165 x US-10-037-667-5
Align seg 1/1 to: US-10-037-667-5 from: 1 to: 498

```

```

64 GATATCCAGATGAGGGCGATGAGCCCATGCCGATCCCGGAGGACCTCTC 113
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
27 AspArgProLysAlaGlyAspSer.....SerLeuGluLysAspPheSe 41
114 C.....ACCACCTCGGAGGACAGCAAGCT 139
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
41 rAspAlaLeuIleGlyProThrValSerThrProAsnSerArgHisSerS 58
140 CCAAGAGTACAGAGTCGGGCCAGTAATGTTAAAGTAGAGACTCAGAGT 189
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
58 erProSerArgSerArgSerAlaAsnSerIleLysValGluMetYrGly 74
190 GATCAAGAGTAATGGCGCTGCCTGTGA..... 216
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
75 AspAspGluSerGlyArgLeuLeuSerHisGluAspArgLeuSerGluLy 91
217 .....ATGAATGGGAAGAATGTGCGGAGGATTTACGAATGC 253
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
91 sGluAspGluIleMetGlyAspSerLeuValGluProLeuGlyTyrC 108
254 TTGATCCCTCGGAGAGAAATGATGCTCCACAGGACCAAGGCAGC 303
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
108 ysAspGlyProGlyGlnAspProHisSerPro..... 118
304 TCGGCTTTGTCGGGAGTTGGAGCATTCGACTTCCTAACGGAAACTAA 353
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
119 .....GlyIleLeuLeuProAsnGlyLysLeuLy 128
354 GTGTGATATCTGTGGATCATTTCCATCGGGCCCAATGTCTCATGTTTC 403
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
128 sCysAspIleCysGlyMetValCysIleGlyProAsnValLeuMetValH 145
404 ACAAGAAGACCACTGGAGAACGGCCCTTCCAGTGCAATCAGTCGGG 453
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
145 lsLysArgSerHisThrGlyGluArgProPheHisCysAsnGlnCysGly 161
454 GCCTCATTCACCCAGAGGACCACTCTCCGGCCACATCAAGTCGATTC 503
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
162 AlaProPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHisSe 178
504 CGGGAGAACCCCTCAATGGCCACTCTGCAACTACGCTCCCGCCGGA 553
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
178 rGlyGluLysProPheLysCysProPheCysAsnTyrAlaCysArgArgA 195
554 GGGACGCCCTCACTGGCCACCTGAGGACCACTCGTGGTAAACCTCAC 603
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
195 rGAspAlaLeuSerGlyHisLeuArgThrHisAlaValGlyLysProYr 211
604 AATGTGGATATTGGCCGAAGCTATAACAGCGAACGCTCTTTAGAGGA 653
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
212 LysCysAsnTyrCysGlyArgSerTyrLysGlnGlnAsnThrLeuGluG 228
654 ACATAAGAGCGCTGCCACAACCTACTTGAAGCATGGGCCCTTCGGGCA 703
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
228 uHisLysGluArgCysHisAsnTyrLeuGlnSerLeu..... 240
704 CACTGTACCCAGCTANTTAAGAAGAACTAAGCACAGTGAATGGCAGAA 753
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
240 ..... 240
754 GACCTGTCAAGATAGGATCAGAGATCTCTCGTGTGGACAGACTAGC 803
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
240 ..... 240
804 AAGTAATGTCGCCAAAGTAAAGCTCTATGCTCAGAAATTTCTTGGG 853
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
241 .SerAsnGluAlaGlnHisLeuProAlaHisProGlyGluTrp...GlyP 256
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
854 ACAAGGCC..... 861
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
256 roGlnGlyGlyAsnCysIleCysThrArgGluLysGlnMetArgLeuSer 272
862 CTGTCCGACACGCCCTTACGAC...AGTGCCACGTACGAGAGGAGAACGA 908

```

```

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
273 LeuAlaAspLeuProYrGluMetAsnSerSerPheGluLysAspValG 289
909 AATGATGAAGTCCACAGTGTGATGACCAACCATCAACACGACCAACT 958
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
289 uIleValSerHisHisProLeuAspThrAlaTyrGlyAsnSerLeuAla 306
959 ACCTGGGGCGGAGTCCCTCGCCCGCTGGTGCAGACGCCCGCGCGGT 1008
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
306 heValGlyGlyPro.....MetArgLeuProProThrAsn 317
1009 .....TCGAGGTGGTCCCGGTATCAGCCCGATGATACACGACG 1052
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
318 CysIleSerGluIleThrProValIleSerSerValIleThrGlnLeu 334
1053 GCGCTCGGAGGACCCCG.....CGTCCAACCACTTCGCCCGCAGGACA 1096
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
334 nProMetGlnGlyArgProAspMetProGlyAsnArgGluAlaAlaGlu 351
1097 GCGCGCTGGAGTACCTGCTGCTCTCCAAGGCCAAGTTGGTCCC... 1143
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
351 lyHisGluAsp.....IleProAsp 357
1144 .....TCGAGCGCGAGCGCTCCCGCAG 1166
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
358 GlyThrGlnIleHisTyrArgGlyArgSerGluHisGlyAlaSerPro 374
1167 CAACAGCTGCCAAGACTCC...ACGGACACCGAGAGCAACACGAGGAGC 1213
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
374 rAsnGlyCysGlnAspSerAsnThrAspThrGluSerAsnHisGluGlu 391
1214 AGCGCAGCGGTCTTATCTACTCAACCAACCATCGCCCGCAGCGCAA 1263
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
391 rGlySer.....GlnAlaThrSerSerArgGlnSer 401
1264 CGCGTGTCTCAAGGAGGACCGCGCTACGAC.....CTGCT 1304
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
402 SerAlaTyrAlaLysGluAspGlnArgProSerAspGlyGlyLeuLeu 418
1305 G.....CGCGCGCTCCGAGAACTCGCAGGACGCGCTCCCGCTGTCA 1348
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
418 uProSerArgSerMetProGlyThrAlaLysGluSerLeuArgValLeu 435
1349 GCACACGGGGAGCAGATGAAGTGTACAAGTGGGAACACTGCCGGGTG 1398
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
435 lyGluAspGlyValGlnValLysValPheLysCysGluHisCysArgVal 451
1399 CTCTTCTCGATCAGTCATGTACACCATCCATGGCGTCCCGCTT 1448
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
452 LeuPheLeuAspHisValMetPheThrIleHisMetGlyCysHisGly 468
1449 CCGTGATCCTTTGAGTCAACATGTGCGGTACACAGCCAGCCAGCCGT 1498
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
468 uArgAspProPheGluCysAsnIleCysGlyTyrHisCysGlnAspArg 485
1499 ACGAGTCTCTCGTCACATACCGGAGGAGGAGCACC 1536
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
485 yrGluPheSerSerHisIleValArgGlyGluHisLys 497

```

us-08-711-417c-165.rapn

Wed Aug 28 10:05:41 2002